In the Specification:

Please amend the specification as shown:

Please insert the following paragraph before paragraph [0002]:

Sequence Listing

The instant application contains a "lengthy" Sequence Listing which has been submitted via CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. Said CD-R, recorded on October 12, 2004, are labeled "Copy 1" and "Copy 2", respectively, and each contains only one identical 592 KB file (SEQ467UT.APP).

Please delete paragraph [0141] and replace it with the following paragraph:

[0141] When designing the siRNA molecules, the targeted region often is selected from a given DNA sequence beginning 50 to 100 nucleotides downstream of the start codon. See, *e.g.*, Elbashir et al,. Methods 26:199-213 (2002). Initially, 5' or 3' UTRs and regions nearby the start codon were avoided assuming that UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP or RISC endonuclease complex. Sometimes regions of the target 23 nucleotides in length conforming to the sequence motif AA(N19)TT **(SEQ ID NO: 141)**(N, any nucleotide), and regions with approximately 30% to 70% G/C-content (often about 50% G/C-content) often are selected. If no suitable sequences are found, the search often is extended using the motif NA(N21). The sequence of the sense siRNA sometimes corresponds to (N19) TT or N21 (position 3 to 23 of the 23-nt motif), respectively. In the latter case, the 3' end of the sense siRNA often is converted to TT. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence composition of the sense and antisense 3' overhangs. The antisense siRNA is synthesized as the complement to position 1 to 21 of the 23-nt motif. Because position 1 of the 23-nt motif is not recognized sequence-specifically by the antisense siRNA, the 3'-most nucleotide residue of the antisense siRNA can be chosen deliberately. However, the penultimate nucleotide of the antisense siRNA (complementary to position 2 of the 23-nt motif) often is complementary to the targeted sequence. For simplifying chemical synthesis, TT often is utilized. siRNAs corresponding to the target motif NAR(N17)YNN, where R is purine (A,G) and Y is pyrimidine (C,U), often are selected.

Respective 21 nucleotide sense and antisense siRNAs often begin with a purine nucleotide and can also be expressed from pol III expression vectors without a change in targeting site. Expression of RNAs from pol III promoters often is efficient when the first transcribed nucleotide is a purine.

Please delete paragraph [0236] and replace it with the following paragraph:

[0236] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer was used to genotype the polymorphism. Other primer design software could be used or one of ordinary skill in the art could manually design primers based on his or her knowledge of the relevant factors and considerations in designing such primers. Table 5 shows PCR primers **(SEQ ID NOS 6-7)** and Table 6 shows **an** extension primers **(SEQ ID NO: 8)** used for analyzing polymorphisms. The initial PCR amplification reaction was performed in a 5 μl total volume containing 1X PCR buffer with 1.5 mM $MgCl_2$ (Qiagen), 200 μM each of dATP, dGTP, dCTP, dTTP (Gibco-BRL), 2.5 ng of genomic DNA, 0.1 units of HotStar DNA polymerase (Qiagen), and 200 nM each of forward and reverse PCR primers specific for the polymorphic region of interest.

Please delete paragraph [0238] and replace it with the following paragraph:

[0238] Once the SAP reaction was complete, a primer extension reaction was initiated by adding a polymorphism-specific MassEXTEND™ primer cocktail to each sample. Each MassEXTEND™ cocktail included a specific combination of dideoxynucleotides (ddNTPs) and deoxynucleotides (dNTPs) used to distinguish polymorphic alleles from one another. Methods for verifying, allelotyping and genotyping SNPs are disclosed, for example, in U.S. Pat. No. 6,258,538, the content of which is hereby incorporated by reference. In Table 6 **(SEQ ID NO: 8)**, ddNTPs are shown and the fourth nucleotide not shown is the dNTP.

Please delete paragraph [0249] and replace it with the following paragraph:

[0249] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer was used to genotype the

polymorphism. Other primer design software could be used or one of ordinary skill in the art could manually design primers based on his or her knowledge of the relevant factors and considerations in designing such primers. Table 8 shows PCR primers **(SEQ ID NOS 9-86, respectively, in order of appearance)** and Table 9 shows extension primers **(SEQ ID NOS 87-125, respectively, in order of appearance)** used for allelotyping the polymorphisms.

Please delete paragraph [0255] and replace it with the following paragraph:

[0255] Four of the SNPs set forth in Table 12 were genotyped as described in Example 2 using the primers and probes set forth in Tables 13 **(SEQ ID NOS 126-133, respectively, in order of appearance)** and 14 **(SEQ ID NOS 134-137, respectively, in order of appearance)**. None of the four SNPs genotyped showed a significant association with breast cancer. See Table 15.

Please delete Table 16 and replace it with the following Table:

Table 16: Duplex 21-mer siRNAs used for cell transfection

siRNA	siRNA Target	Sequence Specificity	SEQ ID NO:
siKLF1	Targets both forms;	AAGGGUCUCCAAACGUCCACA	**138**
siKLF4	Targets truncated form only; 3' UTR	AAGUAUCACAUUCACAGGAUG	**139**
siKLF1 scrm	Non-homologous scrambled control	AAUGCCACAGUACACCAGUCG	**140**